

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: August 21, 2001, 12:06:43 ; Search time 11.18 Seconds

(without alignments)
962.095 Million cell updates/sec

Title: US-09-486-334-2

Perfect score: 1641

Sequence: 1 MATCIDTCRTGNTQDDSRF.....IPCLTMDQSTYLTEMSPDYVI 314

Scoring table: BLOSUM62

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39.*

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	648.5	39.5	273	1	CYSE_ECOLI	P05796 escherichia
2	648.5	39.5	273	1	CYSE_SALTY	P29647 salmonella
3	624.5	38.1	267	1	CYSE_HAEIN	P43886 haemophilus
4	573.5	34.9	274	1	CYSE_BUCAL	P57162 buchnera ap
5	549.5	33.5	261	1	CYSE_BUCAP	P32003 synchococc
6	430.5	26.2	244	1	CYSE_SYNP7	O56002 synchococc
7	424	25.8	217	1	CYSE_BACSU	O06750 bacillus su
8	420.5	25.6	249	1	CYSE_SYNY3	P74089 staphylocyst
9	399	24.3	216	1	CYSE_STAXY	P77985 staphylococ
10	369.5	22.5	269	1	NIFP_AZOC	P23145 azotobacter
11	365	22.2	171	1	CYSE_HELPY	P71405 helicobacte
12	359	21.9	171	1	CYSE_HELPY	O92K14 helicobacte
13	287	17.5	319	1	SRPH_SYNP7	O59667 synchococc
14	217	13.2	162	1	WCAH_ECOLI	P77358 escherichia
15	164.5	10.0	190	1	MODL_RHILV	P08632 rhizobium 1
16	164.5	10.0	214	1	YA64_METUA	O58464 methanococc
17	160	9.8	203	1	THGA_ECOLI	P04092 saccharomyc
18	156.5	9.5	196	1	YJVA_YEAST	P07464 escherichia
19	153.5	9.4	207	1	YA39_SCHPO	O09707 schizosacch
20	150	9.1	183	1	MODL_RHIME	P28366 rhizobium m
21	146.5	8.9	346	1	LPXD_RICPR	O92ed3 rickettsia
22	136.5	8.3	184	1	MAA_BACSU	P37515 bacillus su
23	133.5	8.1	345	1	LPXD_RICRI	P32202 rickettsia
24	129.5	7.9	182	1	MAA_ECOLI	O66662 aquifex aco
25	127.5	7.8	261	1	LPXA_AQUAE	P31552 pseudomonas
26	127.5	7.8	276	1	TABB_PESZ	P39556 staphylococ
27	126.5	7.7	172	1	THGA_LACLA	P52684 lactococcus
28	120.5	7.3	207	1	WCAH_ECOLI	O57752 methanococc
29	117.5	7.2	159	1	WCAH_ECOLI	P71240 escherichia
30	117.5	7.2	182	1	WCAH_ECOLI	P72215 proteus mir
31	115.5	7.0	267	1	LPXA_PROMI	P43887 haemophilus
32	115	7.0	262	1	LPXA_HAEIN	P32201 yersinia en
33	114.5	7.0	262	1	LPXA_YEREN	

ALIGNMENTS

RESULT	ID	STANDARD	PRT	273 AA.
1	CYSE_ECOLI			
34	112.5	6.9	456	1
35	112	6.8	116	1
36	112	6.7	456	1
37	110	6.7	209	1
38	108	6.6	456	1
39	106.5	6.5	340	1
40	105.5	6.4	341	1
41	104.5	6.4	171	1
42	103.5	6.3	275	1
43	103	6.3	209	1
44	103	6.3	210	1
45	102.5	6.2	210	1
1	CYSE_ECOLI			
AC	P05796:			
DT	01-NOV-1988 (rel. 09, Created)			
DT	01-NOV-1988 (rel. 09, Last sequence update)			
DT	30-MAY-2000 (rel. 39, Last annotation update)			
DE	SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).			
GN	CYSE.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OX	NCBI_TaxID=562;			
1	SEQUENCE FROM N.A.			
RA	MEDLINE=88009872; PubMed=3309158;			
RT	Denk D., Boeck A.;			
RT	"L-cysteine biosynthesis in Escherichia coli: nucleotide sequence and			
RT	expression of the serine acetyltransferase (cysE) gene from the wild-			
RT	type and a cysteine-excreting mutant.";			
RL	J. Gen. Microbiol. 133:515-525(1987).			
1	SEQUENCE FROM N.A.			
RC	STRAIN=K12;			
RC	MEDLINE=90211342; PubMed=2108679;			
RA	Tei H., Murata K., Kimura A.;			
RT	"Structure and expression of cysX, the second gene in the Escherichia			
RT	coli K-12 cys locus.";			
RT	Biochem. Biophys. Res. Commun. 167:948-955(1990).			
1	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / MG1655;			
RC	MEDLINE=94316500; PubMed=8041620;			
RA	Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;			
RT	"Analysis of the Escherichia coli genome. V. DNA sequence of the			
RT	region from 76.0 to 81.5 minutes.";			
RT	Nucleic Acids Res. 22:2576-2586(1994).			
1	CHARACTERIZATION.			
RA	MEDLINE=91099514; PubMed=2125278;			
RT	Wigley D.B., Derrick J.P., Shaw W.V.;			
RT	"The serine acetyltransferase from Escherichia coli. Over-expression,			
RT	purification and preliminary crystallographic analysis.";			
RT	FEBS Lett. 277:267-271(1990).			
1	SUBUNIT.			
RA	MEDLINE=20085066; PubMed=10617639;			
RT	Hindson V.J., Moody P.C., Rowe A.J., Shaw W.V.;			
RT	"Serine acetyltransferase from Escherichia coli is a dimer of			
RT	trimers.";			
RL	J. Biol. Chem. 275:461-466(2000).			
1	CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-			
1	ENZIME REGULATION: SENSITIVE TO FEEDBACK INHIBITION BY L-CYSTEINE.			
1	PATHWAY: CYSTEINE BIOSYNTHESIS.			
1	SUBUNIT: HOMOHETEROMER. DIMER OF A HOMOTRIMER.			

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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 CC -----
 CC EMBL: M15745; AAA23648.1; -
 CC EMBL: M34333; AAA23659.1; -
 CC EMBL: U00039; AAB18584.1; -
 CC EMBL: AB000436; AAC76631.1; -
 CC PIR: A27896; XYESCA.
 CC PIR: A34563; A34563.
 CC ECODBASE: H029.3; 6TH EDITION.
 CC Ecogene: EG10187; CYSE.
 CC InterPro: IPR001451; -
 CC Pfam: PF00132; hexapep; 2.
 CC PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 CC Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat.
 CC SEQUENCE 273 AA; 29316 MW; 466EB898750EF709 CRC64;
 SQ
 Query Match 39.5%; Score 648.5; DB 1; Length 273;
 Best Local Similarity 50.8%; Pred. No. 3.1e-44;
 Matches 132; Conservative 51; Mismatches 72; Indels 5; Gaps 2;
 Oy 43 EDDDDVWIKMLEAKSDVQEPILSNYYVASTSHRSLSLAHILSVKLSNLTSPNTL 102
 Db 4 EELEIYWNKIKAKRLADCEPMLASFYHATLKHNLSALSYMLANKLSPIPAIAT 63
 Oy 103 FELFISVLEESPEIESTKODLIAVKEKDPACISYVCFEGFLCAQHRIAHNTLMQ 162
 Db 64 REVEEAADPEMIAASACDIOAVRTDPADVKTSTPLLYLKGFHALQAVRIGHWLMQ 123
 Oy 163 NKRIVALLIQRVSEFVNDIHFGAKIGKILLDHATGVVIGETAVGVGNVSLHGVTIG 222
 Db 124 GRBALAIFLQNOVSFQVDIHPAKIGRIMLDHATGVIGETAVIGEDVSILOSVTIG 183
 Oy 223 GTGKSGDRHPRKIGDGVILGAGSCILGNTITIGEGAKIGSGSVVYKDVPAVTAAGNPARL 282
 Db 184 GTGKSGDRHPRKIREGMIGAGAKILGNTIEVGRGAKIGAGSVVLQVPVPHHTAAGVPART 243
 Oy 283 IGGKENPRKHDKIPCLTMDQ 302
 Db 244 VGRKPS---DK-PSMDMDQ 258
 RESULT 2
 CYSE_SALTY STANDARD; PRT; 273 AA.
 ID CYSE_SALTY P29847;
 AC P29847;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
 GN CYSE.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 NCBI_TaxID=602;
 OX NCB1_TaxID=602;
 RN NCB1_TaxID=602;
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RA Sivaprasad A.V., Kuczek E.S., Bowden C.S., Rogers G.E.;
 RL Submitted (MAY-1991) to the EMBL/GenBank/DDAI databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Rogers G.E.;

RT "Cysteine biosynthesis in transgenic animals.";
 RL Patent number GB2227243, 25-JUL-1990.
 CC -1- CATALYTIC ACTIVITY: ACETYL-CoA + L-SERINE = CoA + O-ACETYL-L-
 CC SERINE.
 CC -1- ENZYME REGULATION: SENSITIVE TO FEEDBACK INHIBITION BY L-CYSTEINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBUNIT: HOMODIMER. DIMER OF A HOMOTRIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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 CC -----
 CC EMBL: X59594; CAA42163.1; -
 CC EMBL: A00198; CAA00039.1; -
 CC PIR: S29568; S29568.
 CC StyGene; SG10073; CYSE.
 CC InterPro: IPR001451; -
 CC Pfam: PF00132; hexapep; 2.
 CC PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 CC Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat.
 CC SEQUENCE 273 AA; 29291 MW; 6A5736B56FBD25B CRC64;
 SQ
 Query Match 39.5%; Score 648.5; DB 1; Length 273;
 Best Local Similarity 51.2%; Pred. No. 3.1e-44;
 Matches 133; Conservative 50; Mismatches 72; Indels 5; Gaps 2;
 Oy 43 EDDDDVWIKMLEAKSDVQEPILSNYYVASTSHRSLSLAHILSVKLSNLTSPNTL 102
 Db 4 EELEIYWNKIKAKRLADCEPMLASFYHATLKHNLSALSYMLANKLSPIPAIAT 63
 Oy 103 FELFISVLEESPEIESTKODLIAVKEKDPACISYVCFEGFLCAQHRIAHNTLMQ 162
 Db 64 REVEEAADPEMIAASACDIOAVRTDPADVKTSTPLLYLKGFHALQAVRIGHWLMQ 123
 Oy 163 NKRIVALLIQRVSEFVNDIHFGAKIGKILLDHATGVVIGETAVGVGNVSLHGVTIG 222
 Db 124 GRBALAIFLQNOVSFQVDIHPAKIGRIMLDHATGVIGETAVIGEDVSILOSVTIG 183
 Oy 223 GTGKSGDRHPRKIGDGVILGAGSCILGNTITIGEGAKIGSGSVVYKDVPAVTAAGNPARL 282
 Db 184 GTGKSGDRHPRKIREGMIGAGAKILGNTIEVGRGAKIGAGSVVLQVPVPHHTAAGVPART 243
 Oy 283 IGGKENPRKHDKIPCLTMDQ 302
 Db 244 VGRKPS---DK-PSMDMDQ 258
 RESULT 3
 CYSE_HAEIN STANDARD; PRT; 267 AA.
 ID CYSE_HAEIN P43886;
 AC P43886;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
 GN CYSE OR H10606.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 NCBI_TaxID=127;
 OX NCB1_TaxID=127;
 RN NCB1_TaxID=127;
 RP SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RA MEDLINE=95350630; PubMed=7542800;
 RX Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-T., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrman J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT Influenzae Rd";
 RL Science 269:496-512(1995).
 CC -1- CATALYTIC ACTIVITY: ACETYL-CoA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LEPA/NODL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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 CC -----
 CC EMBL: U32743; AAC22265.1; -
 CC DR TIGR: H10606; -
 DR Interpro: IPR001451; -
 DR Pfam: PF00132; hexapep; 2.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 KW Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.
 SQ SEQUENCE 267 AA; 29166 MW; 93428DE9D504DBP4 CRC64;

Query Match 38.1%; Score 624.5; DB 1; Length 267;
 Best Local Similarity 48.4%; Pred. No. 2.4e-42;
 Matches 125; Conservative 54; Mismatches 70; Indels 9; Gaps 2;

QY 47 DWIKMLEAKSDVKOEPLISNYTASITSHNSLESALAHILSVKISNLNPSNTLFELEI 106
 DB 4 DWQNHTRQEKALENDPMLASFHSTILKHQWLGALSLANKLANPLMPAISIREII 63
 QY 107 ISVLESPPEIESTKODLAVKERDPAISYVHCFLEFGFLACQAHRAHILMKONKRI 166
 DB 64 EEAQYQNPSTIIDCACDIQVRHRDPAVELMSPPLYLNGFHAIGSYRITHYLMONKRS 123
 QY 167 VALLIQNRSESAVDIHGAKIGKGLLDHATGVYIGTAVGVNVSILHGVTLGTGK 226
 DB 124 LALYLNQISVAVDVIDHPAKIGHGIMEDHATGIYVGETSVIENDVSILOGVTTLGTGK 183
 QY 227 QSGDRHPKIDGVYLIGAGSCILGNTITGEGAKISGSVYVQVDPARTTAVGNPARLIGK 286
 DB 184 ESDGRHPKREGMIGAGAKITLGNIEVGAKTIGANSVYLVNPEYATAGVAPARTV--- 240
 QY 287 ENPRKHDKI--PCLTMDQ 302
 DB 241 ----SODKAKKAPAFDMNQ 254

RESULT 4
 CYSE_BUCAL STANDARD; PRT; 274 AA.
 AC P57162;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
 GN CYSE OR BU054.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 NCBI_TaxID=118099;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TOKYO 1998;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 RT Buchnera sp. APS";
 RT Nature 407:81-86(2000).
 RL Nature 407:81-86(2000).
 CC -1- CATALYTIC ACTIVITY: ACETYL-CoA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LEPA/NODL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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 CC -----
 CC EMBL: AP001118; BAB1277.1; -
 CC DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 KW Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.
 SQ SEQUENCE 274 AA; 30165 MW; 553D252F104B6B61 CRC64;

Query Match 34.9%; Score 573.5; DB 1; Length 274;
 Best Local Similarity 48.9%; Pred. No. 2.6e-38;
 Matches 116; Conservative 47; Mismatches 73; Indels 1; Gaps 1;

QY 48 WIKMLEAKSDVKOEPLISNYTASITSHNSLESALAHILSVKISNLNPSNTLFELEI 107
 DB 9 IWNKILYVVSFLKEKEPLISDFYOSILQHSFTSSLSYILNKLSTSMISEKKIQGIFD 68
 QY 108 SVLESPPEIESTKODLAVKERDPAISYVHCFLEFGFLACQAHRAHILMKONKRI 167
 DB 69 DYLNDRLSTLNFIVDIDAVKALRPAVDVYLPPLYLKGFALEAYRSHYLMWGKSL 128
 QY 168 ALLIQNRSESAVDIHGAKIGKGLLDHATGVYIGTAVGVNVSILHGVTLGTGKQ 227
 DB 129 SLYLSRISSESVDIHRAAFIGSGVMDHATGIVGCVTIENDVSIHVSITLGTGKGN 188
 QY 228 -SGDHPKIDGVYLIGAGSCILGNTITGEGAKISGSVYVQVDPARTTAVGNPARLI 283
 DB 189 FSQNHPTIRKGVYIGAGAKITLGNIEVSGAKIGASIVLKNPVSVDVYVGPAPKIV 245

RESULT 5
 CYSE_BUCAP STANDARD; PRT; 261 AA.
 AC P32003;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
 GN CYSE.
 OS Buchnera aphidicola (subsp. Schizaphis graminum).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 NCBI_TaxID=98794;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93012960; PubMed=1398077;
 RA Lai C.-Y., Baumann P.;
 RT "Sequence analysis of a DNA fragment from Buchnera aphidicola (an
 RT endosymbiont of aphids) containing genes homologous to dnaG, rpoD,
 RT cyse, and secB";
 RL Gene 119:113-118(1992).
 CC -1- CATALYTIC ACTIVITY: ACETYL-CoA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.

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CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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CC -----
CC EMBL: M90644; AAA73232.1; -
CC PIR: JCI293; JCI293.
CC InterPro: IPR001451; -
CC Pfam: PF00132; hexaped; 2.
CC PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
CC Transferrase: Acyltransferase; Cysteine biosynthesis; Repeat.
CC SEQUENCE 261 AA; 28914 MW; DC02685464A25944 CRC64;

Query Match 33.5%; Score 549.5; DB 1; Length 261;
Best Local Similarity 44.1%; Pred. No. 1.9e-36;
Matches 109; Conservative 53; Mismatches 84; Indels 1; Gaps 1;

QY 47 DWIRKLEAKSKVQKPEPLSNYYASTSHSLBSALAHISVKSINLPSTLFLF 106
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 8 ELNMNMRKHAOKLIKKEPLISNFKYSLNHRKLSGHSCLISDKLSTSMISEKDIYNF 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 107 ISVLESPETIEESTKODLAVKERDPACISYVHCFLGFGFLACQAHRIATLMKONKRI 166
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 68 NKRYANNISTINSVMDIRASGRDPVVKHYLPPLLYLKGFPALEVRYSHTLMNKRE 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 167 VALLIONRVSEFAVDIHPKAGIKGILIDHATGVVIGTAVGDNVSLHGVTLAGGTCK 226
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 128 LSAVLOSRTISTVFSDIHPAASIGSGIMDHAITGIYIGEVIIENDVSIFHSVTLAGGTGS 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 227 QSG-DHHPKIGSGVILGASCLIGNTTIGEGAKIGSGVYVVDVARTAVANPRLTGG 285
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 188 NTGKNHPPIIRKNVTIGAKITLIEVGQVAGSIVLANKIPPEVTVVPAKIHK 247
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 286 KENPRKH 292
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 248 IKNSKNK 254
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
CYSE_SYN7 STANDARD; PRT; 244 AA.
AC 056002;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
OS CYSE.
GN Synecococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96281517; PubMed=8661945;
RA Anandan S., Nalty M.S., Coddell D.E., Golden S.S.;
RT "Identification of two classes of transcriptional regulator genes in
RT the cyanobacterium Synecococcus sp. strain PCC 7942."
RL Arch. Microbiol. 166:58-63(1996).
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
CC SERINE.
CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L41665; AAB38543.1; -
CC InterPro: IPR001451; -
CC Pfam: PF00132; hexaped; 2.
CC PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
CC Transferrase: Acyltransferase; Cysteine biosynthesis; Repeat.
CC SEQUENCE 244 AA; 26453 MW; AB0B50491023EBB1 CRC64;

Query Match 26.2%; Score 430.5; DB 1; Length 244;
Best Local Similarity 48.0%; Pred. No. 4.4e-27;
Matches 85; Conservative 33; Mismatches 56; Indels 3; Gaps 1;

QY 123 DLIAVKENDPACISYVHCFLGFGFLACQAHRIATLMKONKRIALLIONRVSEFAVD 182
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 8 DRIIFEDPPARRNGLEVLCYPEFOALVCHRAHWLQQLPVPRLSHLSRLTGE 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 183 IHPKAGIKGILIDHATGVVIGTAVGDNVSLHGVTLAGGTGKSGDRPKIGDGYLG 242
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 68 IHPGARLGQGFIDHGMGVVIGETATVGDYCLYGVLTGCTGKSGKRHPPLANNVYG 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 243 AGSCILGNTTIGEGAKIGSGSVVVDVARTAVANPRLI---GKENPRKHDKTP 296
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 128 AGAVYLNIGIENWVRIGAGSVVLRDVPDCTVVGIRVYISGVVVDPLDHSQMP 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
CYSE_BACSU STANDARD; PRT; 217 AA.
AC 006750;
AC 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
OS CYSE OR CYSA.
GN Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94171772; PubMed=7510287;
RA Gagnon Y., Breton R., Putzer H., Pelchat M., Grunberg-Manago M.,
RA Lapointe J.;
RT "Clustering and co-transcription of the Bacillus subtilis genes
RT encoding the aminoacyl-tRNA synthetases specific for glutamate and
RT for cysteine and the first enzyme for cysteine biosynthesis."
RL J. Biol. Chem. 269:7473-7482(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=168;
RX MEDLINE=96051385; PubMed=7584024;
RA Ogasawara N., Nakai S., Yoshikawa H.;
RT "Systematic sequencing of the 180 kilobase region of the Bacillus
RT subtilis chromosome containing the replication origin."
RL DNA Res. 1:1-14(1994).
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
CC SERINE.
CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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CC -----
CC EMBL: Y07614; CAA68887.1; -
CC InterPro: IPR001451; -
CC Pfam: PF00132; hexapep.2.
CC PROSITE: PS00101; HEXAPEP_TRANSFERRASES; FALSE_NEG.
CC Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat.
CC SEQUENCE 216 AA; 24000 MW; 728FE804A0D7282C CRC64;

Query Match 24.3%; Score 399; DB 1; Length 216;
Best Local Similarity 40.6%; Pred. No. 1.1e-24;
Matches 88; Conservative 41; Mismatches 68; Indels 20; Gaps 5;

QY 115 EIEETKODLIVAKERDPACISVHCFGLFGFLACQAHRIAHITLMKONRKIVALLIONR 174
DB 3 KLLKRIKODVNVVFPQDPAARTLLEIVTSYAGVHAWSHLLAHLYKKKKYVLA RL I SQ 61
QY 175 VSESF-ANDIHGAKIGKILDHATGVVIGETAVGVGNVSLHGVTLGGTGKSGDRHP 233
DB 62 VRFETGIEIHGAGQIGRLFDHGMGVVIGETCRIGDNVITYGVTLGGTGKSGDRHP 121
QY 234 KIGDGVILGAGSCILGNTIGEGAKIGSGVYVKDVPARTAVGNPARIIGKRNPRK- 291
DB 122 DIGDNLVLAAGKAVGNTITINANNVIGANSVVLNSVPSYTVGIGPHIV--KQGRRIIG 179
QY 292 ---HDKIPCLMDQTSYLTE-----WSDYVI 314
DB 180 KTFEDHRLNLPDPIYEQLEKLEKTRNGEIODDYII 216

RESULT 10
NIFP_AZOCH STANDARD; PRT; 269 AA.
AC P23145;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE PROBABLE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
GN NIFP.
OS Azotobacter chroococcum mcd 1.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OX Azotobacter.
RX NCB1_TaxID=355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91358323; PubMed=1885524;
RA Evans D.J., Jones R., Woodley P.R., Milborn J.R., Robson R.L.;
RT "Nucleotide sequence and genetic analysis of the Azotobacter
RT chroococcum nifuswzm gene cluster, including a new gene (nifp) which
RT encodes a serine acetyltransferase.";
RL J. Bacteriol. 173:5457-5469(1991).
CC -1- FUNCTION: PROBABLE SERINE ACETYLTRANSFERASE REQUIRED FOR
CC OPTIMIZING THE EXPRESSION OF NITROGENASE ACTIVITY. NIFP MAY BE
CC REQUIRED TO BOOST RATES OF SYNTHESIS OR INTRACELLULAR
CC CONCENTRATIONS OF CYSTEINE OR METHIONINE.
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
CC SERINE.
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
CC -----
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CC or send an email to license@isb-sib.ch).

CC -----
CC EMBL: M60090; AAA22162.1; -

DR PIR: D43706; D43706.
DR InterPro: IPR001451; -
DR Pfam: PF00132; hexapep.2.
DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
DR Ntrogen fixation; Transferrase; Acyltransferase; Repeat;
KW Cysteine biosynthesis.
KM Cysteine biosynthesis.
SQ SEQUENCE 269 AA; 28578 MW; E0BBCC98266FDBB CRC64;

Query Match 22.5%; Score 369.5; DB 1; Length 269;
Best Local Similarity 42.6%; Pred. No. 3.2e-22;
Matches 83; Conservative 28; Mismatches 63; Indels 21; Gaps 4;

QY 116 IIEETKODLIVAKERDPACISVHCFGLFGFLACQAHRIAHITLMKON-----RKIVALL 169
DB 3 LIAWRKIDICVFERDPAARTLLEIVTSYAGVHAWSHLLAHLYKKKKYVLA RL I SQ 62
QY 170 LIONRSESEFAVDIHGAKIGKILDHATGVVIGETAVGVGNVSLHGVTLGGTGKSG 229
DB 63 LVSN-----VDIHGAVIGARFFIDHGACVYIGETAEIGRDVTLHGVTGGTGANG 115
QY 230 DRHFKIGDVLGAGSCILGNTIGEGAKIGSGVYVKDVPARTAVGNPARI-----GG 285
DB 116 KRHPTLSDVVLVAGAKILSPITIGANARVANSVVDVPECTVVGIPKVKLRAG 175
QY 286 KENP---RKHKRIP 296
DB 176 QLNRYGIDLHHLIP 190

RESULT 11
CYSE_HELPY STANDARD; PRT; 171 AA.
ID CYSE_HELPY
AC P71405;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
GN CYSE OR HP1210.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OX Helicobacter.
RX NCB1_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC 49503 / 60190;
RA Peek R.M., Thompson S.A., Atherton J.C., Blaser M.J., Miller G.G.;
RT "Expression of a novel ulcer-associated gene, *icea*, by *H. pylori*
RT following contact with gastric epithelium.";
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=26695 / ATCC 700392;
RA MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kellavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Letous B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.W., Fujii C., Bowman C., Wathey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen *Helicobacter*
RT *pylori*.";
RL Nature 388:539-547(1997).
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
CC SERINE.
CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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CC or send an email to license@isb-sib.ch).

DR EMBL: U43917; AAB07027.1; -
DR EMBL: AE000626; AAD08254.1; -
DR TIGR: HP1210; -
DR InterPro: IPR001451; -
DR Pfam: PF00132; hexapep. 2.
DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
KW Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat.
FT VARIANT 5 5 S -> F (IN STRAIN 60190).
FT VARIANT 110 110 K -> R (IN STRAIN 60190).
FT VARIANT 162 162 S -> T (IN STRAIN 60190).
SQ SEQUENCE 171 AA; 18342 MW; 28646D539C2250C3 CRC64;

Query Match 22.2%; Score 365; DB 1; Length 171;
Best Local Similarity 45.2%; Pred. No. 4.1e-22;
Matches 71; Conservative 31; Mismatches 55; Indels 0; Gaps 0;

QY 127 VKERDPACISYVHCFLGKFLACQAHRIHTLMKONKRIYALLIONRSESPAVDIHPG 186
DB 11 VLQEDPARAKKWEVLLIPGIIHALCYRLAHAKRRFYFARLALSQARITTEIHPG 70

QY 187 AKIGKGLIDHATGVVIGETAVVGDVNSILHGYTLGGTGKSGDRHPIGDIYLGAGSC 246
DB 71 AKIGRGLFIDHGMGVVIGETETIGDDVTIYHGYTLGGTGKGRHPTLGNRVYVAGAK 130

QY 247 ILGNITIGEGAKIGSGSVYKDVDPARTTAVGNPARI 283
DB 131 VLGAICVDVYKIGANNAVLSDLPTGSTAVASAKRTI 167

RESULT 12
CYS_EHELPJ STANDARD; PRT; 171 AA.
AC 092K14;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
GN CYS_E OR JHP1133.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan A., Guild B.C., deJonge B.L., Camel G.,
RA Tummalo P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Voyis G.F.,
RA Trust T.J.;
RT Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RT Nature 397:176-180(1999).
RL Nature 397:176-180(1999).

CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
CC SERINE.
CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYS_E/LACA/LPXA/NODL FAMILY OF
CC ACETYLTRANSFERRASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).

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DR EMBL: AE001541; AAD06715.1; -
DR InterPro: IPR001451; -
DR Pfam: PF00132; hexapep. 4.
DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
KW Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat.
SQ SEQUENCE 171 AA; 18354 MW; 2872B759C3AC14A CRC64;

Query Match 21.9%; Score 359; DB 1; Length 171;
Best Local Similarity 44.6%; Pred. No. 1.2e-21;
Matches 70; Conservative 31; Mismatches 56; Indels 0; Gaps 0;

QY 127 VKERDPACISYVHCFLGKFLACQAHRIHTLMKONKRIYALLIONRSESPAVDIHPG 186
DB 11 VLQEDPARAKKWEVLLIPGIIHALCYRLAHAKRRFYFARLALSQARITTEIHPG 70

QY 187 AKIGKGLIDHATGVVIGETAVVGDVNSILHGYTLGGTGKSGDRHPIGDIYLGAGSC 246
DB 71 AKIGRGLFIDHGMGVVIGETETIGDDVTIYHGYTLGGTGKGRHPTLGNRVYVAGAK 130

QY 247 ILGNITIGEGAKIGSGSVYKDVDPARTTAVGNPARI 283
DB 131 VLGAICVDVYKIGANNAVLSDLPTGSTAVASAKRTI 167

RESULT 13
SRP_SINP7 STANDARD; PRT; 319 AA.
AC 059967;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SERINE ACETYLTRANSFERASE, PLASMID (EC 2.3.1.30) (SAT).
GN SRP.
OS Synecoccus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synecoccus.
OC Plasmid pANL.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95327059; PubMed=7603442;
RA Nicholson M.L., Gaasenbeek M., Landenbach D.E.;
RT "Two enzymes together capable of cysteine biosynthesis are encoded on
RT a cyanobacterial plasmid."
RT Mol. Gen. Genet. 247:623-632(1995).
RL Mol. Gen. Genet. 247:623-632(1995).
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
CC SERINE.
CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE CYS_E/LACA/LPXA/NODL FAMILY OF
CC ACETYLTRANSFERRASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).

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DR EMBL: U23436; AAB6726.1; -
DR InterPro: IPR001451; -
DR Pfam: PF00132; hexapep. 2.
DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; FALSE_NEG.
KW Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat; Plasmid.
SQ SEQUENCE 319 AA; 34570 MW; 00BB74D8AAB1E70 CRC64;

Query Match 17.5%; Score 287; DB 1; Length 319;

```
Best Local Similarity    30.9% ; Pred.No.1,36-15;
Matches   88; Conservative     32; Mismatches 101; Indels      64; Gaps          8)

QY       47 DWMIKMLEAKSDVKEPILSNVTYYASTSHRSLSALAHLSV-----KLS---- 93
           | :| :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB        19 DSIVALSQASTDPPLPHHLLSDOFY-PLPSRESLGLHLGRLSVLPFRHGDEPELEETT 77
OY       94 -----NLU-----PSMT-----PFELFISYLEKSPE 115
           ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB        78 HYFLGTLDKTLLMLNEQRRELMLOHTYTQGTPENPAVLSSQHASELTQLAFAQLPEIRK 137
OY       116 IESTKODLIAVERKPACISTYHCFLGFGLACQAHRIATMKNRKITALIIONRY 175
           :::::||| | ||| | | | | | | | | | | | | | | | | | | | | | | |
DB        138 LIDS--DVNAVALGPAAQSISELFECYPGITATTFFRHLARLYOLODPLPARITAEVS 194
OY       176 SESAVNDIHGAIGSGILLDHNTAGVGVEGVADVANDSYSLHGYTLGG-----TGR-- 226
           ||||||||| | | | | | | | | | | | | | | | | | | | | | | |
DB        195 HSETGIDIHGAAILGSFPFDIMETGTVIECTVIDRRITYQTIALKAASPRDETALI 254
OY       227 QSGDRHPKPIDGVLIAIGSCIIIGNTIIGEGANIGSGVVADVA 271
           : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
DB        255 KGARRHEIVEDDYIYAAGATLLGRITVGSGSTIGGNVMLTRSVP 299

RESULT_14
WCAB_ECOLI                STANDARD;             PRT;              162 AA.
ID _WCAB_ECOLI
AC P77558;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, last sequence update)
DI 01-OCT-2000 (Rel. 40, Last annotation update)
DE PUTATIVE COLANIC ACID BIOSYNTHESIS ACETYLTRANSFERASE WCAB
DE (EC 2.3.1.-).
GN WCAB.
GC Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxId=562;
LN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=96326333; PubMed=8759852;
RA Stevenson G., Andrianopoulos K., Hobbs M., Reeves P.R.;
RT "Organization of the Escherichia coli K-12 gene cluster responsible
RN for production of the extracellular polysaccharide colanic acid.";
J. Bacteriol. 178:4885-4893(1996).
LN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-N.K12 / MG1655;
RX MEDLINE=97426517; PubMed=9278503;
RA Blatter F.R., Plunkett G.III, Bloch C.A., Perna N.T., Burland V.,
RN Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
MA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12." ;
RN Science 277:1453-1474(1997).
LN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=97251358; Pubmed=9097040;
RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T.,
RN Isoino K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizubuchi K., Mori H., Mori T., Motomura K.,
RN Nakabe S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
RA Sakata N., Sampei G., Seki Y., Sivasanadaran S., Tagami H.,
RN Takeida J., Takemoto K., Wada C., Yamamoto Y., Horichi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RN corresponding to the 40.1-50.0 min region on the linkage map." ;
DNA Res. 3:379-392(1996).
CC -1- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF THE SLIME POLYSACCCHARIDE
CC COLANIC ACID.
CC SIMILARITY: BELONGS TO THE CYSE/LACA/IPXA/NODL FAMILY OF
CC ACTYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIY]-G-X(4.).
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CC      -----
DR      EMBL; U38473; AAC77837.1; .
DR      EMBL; AE000295; AAC75119.1; .
DR      EMBL; D90843; BAAL5911.1; .
DR      EcoGene; EG13570; weaB.
DR      InterPro; IPR001451; .
DR      Pfam; PF00132; hexapep; 2.
DR      PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
KW      Lipopolysaccharide biosynthesis; Transferase; Acyltransferase; Repeat.
SQ      SEQUENCE 162 AA; 17615 MW; F2462P836F3FB3AD CRC64;

Query Match 13.2%; Score 217; DB 1; Length 162;
Best Local Similarity 37.1%; Pred. No. 1,8e-10;
Matches 52; Conservative 24; Mismatches 54; Indels 10; Gaps 4.

OY 152 AHRIAH--TLMKO-----NKKYVALLIQRVSES--FAVDIHPEAKIGKGIILDHATGVY 202
DB 20 AYRAHHCSYWRKKKNVNLINMAAPLLVLYRITTECFEYEQAAATIGRTTHHGVAV 79
OY 203 IGETAVVGDVNVSLIHGVTLLGTGKSGSDRHPKIGDGVILGAGSCILLITIGESAKTGG 262
DB 80 INKNVVAAGDDPTIRHGVTIGTIGRGADN-MACPHTGNGVELGANVILLIDITLGINNVTVGAG 138
OY 263 SVYVKDYPAFTAVGNPARL 262
DB 139 SVLDISVDPNALVYGEKARV 158

RESULT 15
NODL_RHLV STANDARD; PRT; 190 AA.
ID NODL_RHLV
AC P08632;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, last sequence update)
DT 01-JUN-1994 (Rel. 29, last annotation update)
DE MODULATION PROTEIN L (EC 2.3.1.1.-).
GN NODL.
OS Rhizobium leguminosarum (biovar viciae).
OC Plasmid sym PRL1J1.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=387;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=248;
RX MEDLINE=88246045; PubMed=3132583;
RA Surin B.P., Downie J.A.;
RT "Characterization of the Rhizobium leguminosarum genes nodL and
RT involved in efficient host-specific nodulation.";
RL Mol. Microbiol. 2:173-183(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92003664; PubMed=2562395;
RA Canter Cremers H.C.J., Spaink H.P., Wijffes A.H.M., Pees E.,
RA Willeman C.A., Okker R.J.H., Lugtenberg B.J.J.;
RT "Additional nodulation genes on the Sym Plasmid of Rhizobium
RT leguminosarum biovar viciae.";
RL Plant Mol. Biol. 13:165-174(1989).
RN [3]
RP SIMILARITY TO OTHER MEMBER OF THE CYSE/LACA/NODL FAMILY.
RX MEDLINE=90136094; PubMed=2615659;
RA Downie J.A.;
RT "The nodL gene from Rhizobium leguminosarum is homologous to the
RT acetyl transferases encoded by laca and cyste.";
```



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RL Mol. Microbiol. 3:1649-1651(1989).
CC -1- FUNCTION: ACETYLTRANSFERASE IMPLICATED IN THE O-ACETYLATION OF
CC NOD FACTORS.
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
CC -----
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CC -----
DR EMBL; X17557; CAA35590.1; -
DR EMBL; Y00548; CAA68625.1; -
DR PIR; S01039; S01039.
DR PIR; S07000; S07000.
DR InterPro: IPR001451; -
DR Pfam: PF00132; hexapep; 2.
DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
DR Plasmid; Nodulation; Transferase; Acyltransferase; Repeat.
KW SEQUENCE 190 AA; 20105 MW; 2AC4E82D6EDF48C CRC64;
SQ

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Query Match          10.0%; Score 164.5; DB 1; Length 190;
Best Local Similarity 42.7%; Pred. No. 3.1e-06;
Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3;

QY 193 ILIDHATGVVIGETAVVGNVSI-----HGVTLGSTGKQSGDRHFKTGDGVILGAGSCI 247
   :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 89 VILDVA-AVTIGDGFATGPAVOIYTADHDEPQAGLQLG-REVSTGRHAWIGGAI 146
   | :||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 248 LGNITGEGAKTGGSVVVKDVPARTAVGNFARLIGKENPR 290
   | :||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 147 LQGVITGDHVAVIGAGSVVTRDVPAGSTAMGNPARYKAGGRLPK 189

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Search completed: August 21, 2001, 12:09:35
Job time: 172 sec

